

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING ERROR REPORT**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: 10/563,194  
Source: IFwp  
Date Processed by STIC: 1/13/06

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/563,194</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor <b>after</b> creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line <b>not exceed</b> 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do <b>not</b> use tab codes between numbers; use <b>space characters</b> , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was <b>not saved</b> in ASCII(DOS) text, as <b>required</b> by the Sequence Rules. <b>Please ensure your subsequent submission is saved in ASCII text.</b>	
5 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. <b>Per Sequence Rules, each n or Xaa can only represent a single residue.</b> Please present the <b>maximum</b> number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for <b>each</b> skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to <b>include</b> the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If <b>intentional</b> , please insert the following lines for <b>each</b> skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is <b>required</b> when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) <input type="checkbox"/> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can <b>only</b> represent a single <u>nucleotide</u> ; "Xaa" can <b>only</b> represent a single <u>amino acid</u>	



IFWP

Show <110> only  
Once.

delete  
extra <110>s.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/563,194

DATE: 01/13/2006

TIME: 10:18:21

Input Set : A:\SEQUENCE LISTING.txt-9663.66USWO.txt  
Output Set: N:\CRF4\01132006\J563194.raw

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3 <110> APPLICANT: JENSEN, Jens Stougaard
W--> 4 <110> APPLICANT: MADSEN, Lene Heegaard
W--> 5 <110> APPLICANT: RADUTOIU, Elena Simona
W--> 6 <110> APPLICANT: MADSEN, Esben Bjorn
W--> 7 <110> APPLICANT: SANDAL, Niels Norgaard
9 <120> TITLE OF INVENTION: Nod-factor perception
11 <130> FILE REFERENCE: 09663.0066USWO
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/563,194
14 <141> CURRENT FILING DATE: 2006-01-03
16 <150> PRIOR APPLICATION NUMBER: PCT/DK2004/000478
17 <151> PRIOR FILING DATE: 2004-07-02
19 <150> PRIOR APPLICATION NUMBER: PA 2003 01010 DK
20 <151> PRIOR FILING DATE: 2003-07-03
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27 <211> LENGTH: 45
28 <212> TYPE: DNA
29 <213> ORGANISM: Lotus japonicus
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36 <211> LENGTH: 29
37 <212> TYPE: DNA
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44 <210> SEQ ID NO: 3
45 <211> LENGTH: 21
46 <212> TYPE: DNA
47 <213> ORGANISM: Lotus japonicus
49 <400> SEQUENCE: 3
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53 <210> SEQ ID NO: 4
54 <211> LENGTH: 39
55 <212> TYPE: DNA
56 <213> ORGANISM: synthetic sequence
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60 <221> NAME/KEY: misc_feature
61 <222> LOCATION: (1)..(39)
62 <223> OTHER INFORMATION: Oligo dT primer
64 <400> SEQUENCE: 4
65 gaccacgcgt atcgatgtcg actttttttt tttttttv 39

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Does Not Comply  
Corrected Diskette Needed

ppr1,6-7

initial <213> response. See item 10 on  
Error Summary  
Sheet.

**RAW SEQUENCE LISTING** DATE: 01/13/2006  
**PATENT APPLICATION:** US/10/563,194 **TIME:** 10:18:21

Input Set : A:\SEQUENCE LISTING.txt-9663.66USWO.txt  
 Output Set: N:\CRF4\01132006\J563194.raw

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87 ttgtccccca cttcacaaac atggctgtot tctttcttac ctctggctct ctgagtctt 180
89 ttcttgact cacgttgctt ttcaactaaca tcgcgcgtcg atcagaaaaag attagcgccc 240
91 cagacttttc atgcctgtt gactcaccc tcctctgtga aacatatgtg acatacacag 300
93 ctcagtctcc aaatcttctg agcctgacaa acatatctga tatatttgat atcagtcctt 360
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99 accaaatcca gcttaggtgat agctacgact ttgttcaac cactttatgat gagaacctt 540
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153 caaattcagg caagatagttt aattgcattt gaaatacata tttctgtca gagatgggtga 2160
155 acatccatgc tccgaagctc atattaatgt tggttagctat ttcttttca tctttttggg 2220
157 gtgaatgcgt gttcatgtaa ctcgttaagggtt gtttatattt acagaagtcg tatacgtcgt 2280
  
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**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/563,194**

**DATE: 01/13/2006**  
**TIME: 10:18:21**

**Input Set : A:\SEQUENCE LISTING.txt-9663.66USWO.txt**  
**Output Set: N:\CRF4\01132006\J563194.raw**

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163 <211> LENGTH: 3536	
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165 <213> ORGANISM: Lotus japonicus GIFU	
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172 ccagttgggt tggagagc tattttgtta tgctgacatc tgcaatttgc agggcatcta	180
174 atgattgtca tttcttaaat tattattgtt tgttccgtt tctttaatta tctgttttaa	240
176 tcttcaggc catacaaatt aaaatactag ccaccaccca agacatacta aatgggttag	300
178 tagagggaag ggtaaggctg ataaggatga ctttttattc tataaaattt aggagaattt	360
180 gagcttaagt ggcaaggcaa acgcattac tatacgatt ggctttgtac cagaaacagg	420
182 gaacaaataaa tattttacaa ataagctatt atcatgtcag ctcatttgc caactttgat	480
184 ttgattaaaa attaaatgaa gttgaatttg ttgagctgt ttattatata tgccactgga	540
186 tgttccgca ttcttaagtgc atgttgaaa acatttctac aattgattac gaaggaaaaa	600
188 ttaatcatgg agagaagctt atgtgcgtag ctttgttatt tctgaattga ttctatctgt	660
190 acagtagcat ttagataatg aatgatctt gttctcgcta agcatcaaac caatctctac	720
192 ccttttaaaa ttgcaagaat tataagtcat gcattgaccc aaatcctct gtgttatgc	780
194 cccttaaaaaa tccggcaaga catcaagtta gttgtcatt agggttccac cagctagctg	840
196 acaccttgc taacaactgg ccgtcctaaa gttgggttaag cattacaata ctaaatgcca	900
198 ttttattata ttttgcgcatt gtttatatac ctaagtagga tttgtccaca gtttcttgc	960
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202 atgaaatgac tcctacatga gatacacgaa tctcatcccc atgagttgca gtttgacaga	1080
204 gtacacactt atcaacttgc tggatatata gaaagtctaa ccaatgtatgt cgatccgtat	1140
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208 tattttattt acaatgtgaa tggccatatt ttcaacaat gctgattccc tctgataaag	1260
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218 tgacaaacat atctgatata ttgtatatac gtcccttgc cattgcaaga gccagtaaca	1560
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238 taaccgggac cctcgatata gttactgcc gcagaaagaa ggctctgaat aggactgctt	2160
240 catcagctga gactgctgat aaactacttt ctggagttt aggctatgtt agcaagccaa	2220
242 acgtgtatga aatcgacgag ataatggaa ctacgaagga tttcagcgtt gagtgcaagg	2280
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248 tgaaaactaat ggggtctcc tcaggctatg atggaaactg tttcttgc ttatgtatgc	2460
250 ctgaaaatgg gtctcttgc ggtgttgc tctccaatgc ttccaggacc ccaaactccc	2520
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PATENT APPLICATION: US/10/563,194

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Input Set : A:\SEQUENCE LISTING.txt-9663.66USWO.txt  
Output Set: N:\CRF4\01132006\J563194.raw

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256	actcgaaatt	caaggccaag	atagcgaatt	tcgcattgc	cagaacttcg	accaacccca	2700									
258	tgtgcctaa	aatcgatgtc	ttcgcttcg	gggtgcttct	gatagagttg	ctcacccgaa	2760									
260	ggaaaagccat	gacaaccaag	gagaacggcg	agggtggttat	gctgtgaaag	gatatgtggg	2820									
262	agatcttga	catagaagag	aatagagagg	agaggatcag	aaaatggatg	gatcctaatt	2880									
264	tagagagctt	ttatcatata	gataatgctc	tcagcttgc	atccttagca	gtgaattgca	2940									
266	cagctgataa	gtcttgtct	cgaccctcca	tggctgaaat	tgttcttagc	ctctccccc	3000									
268	tcactcaaca	atcatctaac	cccacattag	agagatcctt	gacttcttct	gggttagatg	3060									
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272	cagttctca	tcaaattgtat	caagatgcac	tttggttgcg	tggttactat	tacatttta	3180									
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298	Leu	Thr	Leu	Leu	Phe	Thr	Asn	Ile	Ala	Ala	Arg	Ser	Glu	Lys	Ile	Ser
299					20		25					30				
302	Gly	Pro	Asp	Phe	Ser	Cys	Pro	Val	Asp	Ser	Pro	Pro	Ser	Cys	Glu	Thr
303						35		40			45					
306	Tyr	Val	Thr	Tyr	Thr	Ala	Gln	Ser	Pro	Asn	Leu	Leu	Ser	Leu	Thr	Asn
307						50		55			60					
310	Ile	Ser	Asp	Ile	Phe	Asp	Ile	Ser	Pro	Leu	Ser	Ile	Ala	Arg	Ala	Ser
311						65		70			75			80		
314	Asn	Ile	Asp	Ala	Gly	Lys	Asp	Lys	Leu	Val	Pro	Gly	Gln	Val	Leu	Leu
315						85		90			95					
318	Val	Pro	Val	Thr	Cys	Gly	Cys	Ala	Gly	Asn	His	Ser	Ser	Ala	Asn	Thr
319						100		105			110					
322	Ser	Tyr	Gln	Ile	Gln	Leu	Gly	Asp	Ser	Tyr	Asp	Phe	Val	Ala	Thr	Thr
323						115		120			125					
326	Leu	Tyr	Glu	Asn	Leu	Thr	Asn	Trp	Asn	Ile	Val	Gln	Ala	Ser	Asn	Pro
327						130		135			140					
330	Gly	Val	Asn	Pro	Tyr	Leu	Leu	Pro	Glu	Arg	Val	Lys	Val	Val	Phe	Pro
331						145		150			155			160		
334	Leu	Phe	Cys	Arg	Cys	Pro	Ser	Lys	Asn	Gln	Leu	Asn	Lys	Gly	Ile	Gln
335						165		170			175					
338	Tyr	Leu	Ile	Thr	Tyr	Val	Trp	Lys	Pro	Asn	Asp	Asn	Val	Ser	Leu	Val
339						180		185			190					
342	Ser	Ala	Lys	Phe	Gly	Ala	Ser	Pro	Ala	Asp	Ile	Leu	Thr	Glu	Asn	Arg
343						195		200			205					
346	Tyr	Gly	Gln	Asp	Phe	Thr	Ala	Ala	Thr	Asn	Leu	Pro	Ile	Leu	Ile	Pro
347						210		215			220					

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Input Set : A:\SEQUENCE LISTING.txt-9663.66USWO.txt  
Output Set: N:\CRF4\01132006\J563194.raw

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355 245 250 255  
358 Leu Leu Thr Ala Val Leu Thr Gly Thr Leu Val Tyr Val Tyr Cys Arg  
359 260 265 270  
362 Arg Lys Lys Ala Leu Asn Arg Thr Ala Ser Ser Ala Glu Thr Ala Asp  
363 275 280 285  
366 Lys Leu Leu Ser Gly Val Ser Gly Tyr Val Ser Lys Pro Asn Val Tyr  
367 290 295 300  
370 Glu Ile Asp Glu Ile Met Glu Ala Thr Lys Asp Phe Ser Asp Glu Cys  
371 305 310 315 320  
374 Lys Val Gly Glu Ser Val Tyr Lys Ala Asn Ile Glu Gly Arg Val Val  
375 325 330 335  
378 Ala Val Lys Lys Ile Lys Glu Gly Ala Asn Glu Glu Leu Lys Ile  
379 340 345 350  
382 Leu Gln Lys Val Asn His Gly Asn Leu Val Lys Leu Met Gly Val Ser  
383 355 360 365  
386 Ser Gly Tyr Asp Gly Asn Cys Phe Leu Val Tyr Glu Tyr Ala Glu Asn  
387 370 375 380  
390 Gly Ser Leu Ala Glu Trp Leu Phe Ser Lys Ser Ser Gly Thr Pro Asn  
391 385 390 395 400  
394 Ser Leu Thr Trp Ser Gln Arg Ile Ser Ile Ala Val Asp Val Ala Val  
395 405 410 415  
398 Gly Leu Gln Tyr Met His Glu His Thr Tyr Pro Arg Ile Ile His Arg  
399 420 425 430  
402 Asp Ile Thr Thr Ser Asn Ile Leu Leu Asp Ser Asn Phe Lys Ala Lys  
403 435 440 445  
406 Ile Ala Asn Phe Ala Met Ala Arg Thr Ser Thr Asn Pro Met Met Pro  
407 450 455 460  
410 Lys Ile Asp Val Phe Ala Phe Gly Val Leu Leu Ile Glu Leu Leu Thr  
411 465 470 475 480  
414 Gly Arg Lys Ala Met Thr Thr Lys Glu Asn Gly Glu Val Val Met Leu  
415 485 490 495  
418 Trp Lys Asp Met Trp Glu Ile Phe Asp Ile Glu Glu Asn Arg Glu Glu  
419 500 505 510  
422 Arg Ile Arg Lys Trp Met Asp Pro Asn Leu Glu Ser Phe Tyr His Ile  
423 515 520 525  
426 Asp Asn Ala Leu Ser Leu Ala Ser Leu Ala Val Asn Cys Thr Ala Asp  
427 530 535 540  
430 Lys Ser Leu Ser Arg Pro Ser Met Ala Glu Ile Val Leu Ser Leu Ser  
431 545 550 555 560  
434 Phe Leu Thr Gln Gln Ser Ser Asn Pro Thr Leu Glu Arg Ser Leu Thr  
435 565 570 575  
438 Ser Ser Gly Leu Asp Val Glu Asp Asp Ala His Ile Val Thr Ser Ile  
439 580 585 590  
442 Thr Ala Arg  
443 595  
446 <210> SEQ ID NO: 9

10/563,194 6

from sequence 23

tga aga cag gtg aat tag ttg ctg aat caa agg gcc ttg tag ctt tg	9275
Arg Gln Val Asn Leu Leu Asn Gln Arg Ala Leu Leu Cys	
520 525	530 ← insert
gtgagtc tac atgccccttc tctaaccctta tttacaaacc aatttactcac aatttcgaaa	9335
attttacatg tatatttcaa agctactcag cacaaatgca ttggccctta acttgcttg	9395
cattgcag t ttg aag aag cac tta ata aga gtg atc ctt gtg atg ctc	9443
Leu Lys Lys His Leu Ile Arg Val Ile Leu Val Met Leu	
535 540	

10/563,194 7

<210> 45  
<211> 26  
<212> DNA  
<213> Glycine max

<220>  
<221> misc feature  
<222> (1). (27) do you mean (26)?  
<223> NPR5 gene PCR primers

<400> 45  
ctaatacgac ataccaacaa ctgcag

26

**VERIFICATION SUMMARY** DATE: 01/13/2006  
PATENT APPLICATION: US/10/563,194 TIME: 10:18:22

Input Set : A:\SEQUENCE LISTING.txt-9663.66USWO.txt  
Output Set: N:\CRF4\01132006\J563194.raw

L:4 M:280 W: Numeric Identifier already exists, <110> found multiple times  
L:5 M:280 W: Numeric Identifier already exists, <110> found multiple times  
L:6 M:280 W: Numeric Identifier already exists, <110> found multiple times  
L:7 M:280 W: Numeric Identifier already exists, <110> found multiple times  
L:13 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:1502 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 23  
L:1697 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:1720 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 23